

RESULT 1  
 Y938\_MYCTU  
 ID Y938\_MYCTU Reviewed; 759 AA.  
 AC P71571; O05865;  
 DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.  
 DT 30-MAY-2000, sequence version 2.  
 DT 24-NOV-2009, entry version 67.  
 DE RecName: Full=Putative DNA ligase-like protein Rv0938/MT0965;  
 GN OrderedLocusNames=Rv0938, MT0965; ORFNames=MTCY08D9.01c, MTCY10D7.36c;  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;  
 OC Mycobacterium tuberculosis complex.  
 OX NCBI\_TaxID=1773;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=ATCC 25618 / H37Rv;  
 RX MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,  
 RA Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,  
 RA Tekaiia F., Badcock K., Basham D., Brown D., Chillingworth T.,  
 RA Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,  
 RA Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,  
 RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,  
 RA Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence.";  
 RL Nature 393:537-544(1998).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=CDC 1551 / Oshkosh;  
 RX MEDLINE=22206494; PubMed=12218036;  
 RX DOI=10.1128/JB.184.19.5479-5490.2002;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.E., Haft D.H.,  
 RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,  
 RA Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,  
 RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,  
 RA Fraser C.M.;  
 RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains.";  
 RL J. Bacteriol. 184:5479-5490(2002).  
 CC -!- SIMILARITY: Belongs to the ATP-dependent DNA ligase family.  
 CC -----  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
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 CC -----  
 DR EMBL; BX842575; CAB08492.1; -; Genomic\_DNA.  
 DR EMBL; AE000516; AAK45212.1; -; Genomic\_DNA.  
 DR FIR; B70585; B70585.  
 DR RefSeq; NP\_215453.1; -.  
 DR RefSeq; NP\_335398.1; -.  
 DR PDB; 1VS0; X-ray; 2.40 A; A/B=452-759.  
 DR PDB; 2IRU; X-ray; 1.65 A; A/B=1-300.  
 DR PDB; 2IRX; X-ray; 1.80 A; A=1-300.  
 DR PDB; 2IRY; X-ray; 1.78 A; A/B=1-300.

DR PDB; 2R9L; X-ray; 2.40 Å; A/B=1-300.  
 DR PDBsum; 1VS0; -.  
 DR PDBsum; 2IRU; -.  
 DR PDBsum; 2IRX; -.  
 DR PDBsum; 2IRY; -.  
 DR PDBsum; 2R9L; -.  
 DR GeneID; 885561; -.  
 DR GeneID; 926354; -.  
 DR GenomeReviews; AE000516\_GR; MT0965.  
 DR GenomeReviews; AL123456\_GR; Rv0938.  
 DR KEGG; mtc:MT0965; -.  
 DR KEGG; mtu:Rv0938; -.  
 DR TIGR; MT0965; -.  
 DR TubercuList; Rv0938; -.  
 DR HOGENOM; P71571; -.  
 DR OMA; VDWSQNN; -.  
 DR GO; GO:0005524; F:ATP binding; IEA:UniProtKB-KW.  
 DR GO; GO:0003910; F:DNA ligase (ATP) activity; IEA:InterPro.  
 DR GO; GO:0003896; F:DNA primase activity; IEA:InterPro.  
 DR GO; GO:0006310; P:DNA recombination; IEA:InterPro.  
 DR GO; GO:0006281; P:DNA repair; IEA:InterPro.  
 DR GO; GO:0006269; P:DNA replication, synthesis of RNA primer; IEA:InterPro.  
 DR InterPro; IPR012309; DNA\_ligase\_A\_C.  
 DR InterPro; IPR012310; DNA\_ligase\_A\_M.  
 DR InterPro; IPR002755; DNA\_primase\_S.  
 DR InterPro; IPR014144; LigD\_PE\_domain.  
 DR InterPro; IPR014145; LigD\_pol.  
 DR InterPro; IPR012340; NA-bd\_OB-fold.  
 DR InterPro; IPR014146; NHEJ\_ligase\_lig.  
 DR Gene3D; G3DSA:2.40.50.140; OB\_NA\_bd\_sub; 1.  
 DR Pfam; PF04679; DNA\_ligase\_A\_C; 1.  
 DR Pfam; PF01068; DNA\_ligase\_A\_M; 1.  
 DR Pfam; PF01896; DNA\_primase\_S; 1.  
 DR TIGRFAMs; TIGR02777; LigD\_PE\_dom; 1.  
 DR TIGRFAMs; TIGR02778; ligD\_pol; 1.  
 DR TIGRFAMs; TIGR02779; NHEJ\_ligase\_lig; 1.  
 DR PROSITE; PS50160; DNA\_LIGASE\_A3; 1.  
 PE 1: Evidence at protein level;  
 KW 3D-structure; ATP-binding; Complete proteome; Ligase;  
 KW Nucleotide-binding.  
 FT CHAIN 1 759 Putative DNA ligase-like protein  
 FT Rv0938/MT0965.  
 FT /FTId=PRO\_0000059627.  
 FT ACT\_SITE 481 481 N6-AMP-lysine intermediate (By  
 FT similarity).  
 FT CONFLICT 344 344 C -> R (in Ref. 2; AAK45212).  
 FT TURN 20 22  
 FT HELIX 26 44  
 FT STRAND 50 53  
 FT STRAND 63 65  
 FT STRAND 76 83  
 FT STRAND 86 92  
 FT HELIX 96 104  
 FT STRAND 109 112  
 FT STRAND 114 119  
 FT TURN 121 123  
 FT STRAND 126 140

FT	HELIX	146	162
FT	STRAND	168	171
FT	STRAND	173	175
FT	STRAND	177	187
FT	HELIX	189	206
FT	TURN	208	210
FT	HELIX	217	219
FT	STRAND	221	227
FT	HELIX	229	231
FT	STRAND	246	248
FT	HELIX	257	260
FT	HELIX	270	280
FT	TURN	283	290
FT	HELIX	455	457
FT	STRAND	462	465
FT	TURN	473	475
FT	STRAND	476	479
FT	STRAND	484	492
FT	STRAND	495	500
FT	HELIX	507	509
FT	HELIX	511	513
FT	HELIX	514	519
FT	TURN	520	522
FT	STRAND	524	532
FT	HELIX	542	546
FT	STRAND	555	564
FT	HELIX	574	587
FT	HELIX	600	609
FT	STRAND	614	619
FT	STRAND	629	650
FT	STRAND	662	669
FT	STRAND	672	679
FT	HELIX	685	695
FT	HELIX	696	698
FT	STRAND	704	707
FT	HELIX	711	714
FT	STRAND	717	720
FT	STRAND	725	731
FT	STRAND	743	747
FT	HELIX	753	755

SQ SEQUENCE 759 AA; 83572 MW; 81BD49222EE09E36 CRC64;

Query Match 100.0%; Score 3993; DB 1; Length 759;

Best Local Similarity 100.0%;

Matches 759; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGSASEQRVTLTNADKVLYPATGTTKSDIFDYYAGVAEVLGHIAGRPA	60
Db	1	MGSASEQRVTLTNADKVLYPATGTTKSDIFDYYAGVAEVLGHIAGRPA	60
Qy	61	PAFFFEKQLALSAPPWLSRATVAHRS GTTTP IID SATGLAWIAQQAALE	120
Db	61	PAFFFEKQLALSAPPWLSRATVAHRS GTTTP IID SATGLAWIAQQAALE	120
Qy	121	PGSGELNPGPATRLVFDLDPGEGVMAQLAEVARAVRDLLADIGLVTFPV	180
Db	121	PGSGELNPGPATRLVFDLDPGEGVMAQLAEVARAVRDLLADIGLVTFPV	180

Qy	181	TPLDEFVSSRGATVLAQRVAQRLEQAMPALVTSTMTKSLRAGKVFVDWSQNSGSKTTIAP	240
Db	181	TPLDEFVSSRGATVLAQRVAQRLEQAMPALVTSTMTKSLRAGKVFVDWSQNSGSKTTIAP	240
Qy	241	YSLRGRTHPTVAAPRTWAELDDPALRQLSYDEVLTIRARDGDLERLDADAPVADRLTRY	300
Db	241	YSLRGRTHPTVAAPRTWAELDDPALRQLSYDEVLTIRARDGDLERLDADAPVADRLTRY	300
Qy	301	RRMRDASKTPEPIPTAKPVTGDGNTFVIQEHARRPHYDFRLECDGVLVSWAVPKNLPDN	360
Db	301	RRMRDASKTPEPIPTAKPVTGDGNTFVIQEHARRPHYDFRLECDGVLVSWAVPKNLPDN	360
Qy	361	TSVNHIAHTEDHPLEYATFEGAIPSGEYGAGKVIWDSGTYDTEKFHDDPHTGEVIVNL	420
Db	361	TSVNHIAHTEDHPLEYATFEGAIPSGEYGAGKVIWDSGTYDTEKFHDDPHTGEVIVNL	420
Qy	421	HGGRISGRYALIRTINGDRWLAHRLKNQKQKVFEFDNLAPMLATHGTAVAGLKASQWAFEG	480
Db	421	HGGRISGRYALIRTINGDRWLAHRLKNQKQKVFEFDNLAPMLATHGTAVAGLKASQWAFEG	480
Qy	481	KWDGYRLLEADHGAVRLRSRSGRDVTAIEYQPLRALAEDLADHHVVDLGEAVVLDSSGVP	540
Db	481	KWDGYRLLEADHGAVRLRSRSGRDVTAIEYQPLRALAEDLADHHVVDLGEAVVLDSSGVP	540
Qy	541	SFSQMQRNGRDTRVEFWAFDLYLDGRALLGTRYQDRKLETLANATSLTVPELLPGDG	600
Db	541	SFSQMQRNGRDTRVEFWAFDLYLDGRALLGTRYQDRKLETLANATSLTVPELLPGDG	600
Qy	601	AQAFACSRKHGWEGVIAKRRDSRYQPGRRCASWVKDKHWNTQEVVIGGWAGEGGRSSGV	660
Db	601	AQAFACSRKHGWEGVIAKRRDSRYQPGRRCASWVKDKHWNTQEVVIGGWAGEGGRSSGV	660
Qy	661	GSLLMGIPGPGGLQFAGRVGTGLSERELANLKEMLAPLHDESFPDVPPLPARDAKGITYV	720
Db	661	GSLLMGIPGPGGLQFAGRVGTGLSERELANLKEMLAPLHDESFPDVPPLPARDAKGITYV	720
Qy	721	KPALVAEVRYSEWTPEGRRLQSSWRGLRPDKKPSEVVRE	759
Db	721	KPALVAEVRYSEWTPEGRRLQSSWRGLRPDKKPSEVVRE	759

# RESULT 1

B70585

hypothetical protein Rv0938 - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004

C;Accession: B70585

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry III, C.E.; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: B70585

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-759

A;Cross-references: UNIPROT:P71571; UNIPARC:UPI0000139E3C; GB:295209; GB:AL123456;

NID:g3261750; PIDN:CAB08492.1; PID:e1299776; PID:g3261755

A;Experimental source: strain H37Rv

C;Genetics:

A;Gene: Rv0938

Query Match 100.0%; Score 3993; DB 2; Length 759;  
Best Local Similarity 100.0%;  
Matches 759; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  MGSASEQQRVTLTNADKVLYPATGTTKSDIFDYYAGVAEVLGHIAGR PATKRKPNGVDQ 60
      |||
Db      1  MGSASEQQRVTLTNADKVLYPATGTTKSDIFDYYAGVAEVLGHIAGR PATKRKPNGVDQ 60

Qy     61  PAFFEKQLALSAPPWLSRATVAHRS GTTTPYIIDSATGLAWIAQQAAL EVHVPQWR FVAE 120
      |||
Db     61  PAFFEKQLALSAPPWLSRATVAHRS GTTTPYIIDSATGLAWIAQQAAL EVHVPQWR FVAE 120

Qy    121  PGSGELNPGPATRLVFDLDPGEGVMAQLAEVARAVRDLLADIGLVTFFPV TSGSKGLHL Y 180
      |||
Db    121  PGSGELNPGPATRLVFDLDPGEGVMAQLAEVARAVRDLLADIGLVTFFPV TSGSKGLHL Y 180

Qy    181  TPLDEPVSSRGATVLAKRVAQRLEQAMPALVTSTMTKSLRAGKV FVDWSQNSGSKT TIAP 240
      |||
Db    181  TPLDEPVSSRGATVLAKRVAQRLEQAMPALVTSTMTKSLRAGKV FVDWSQNSGSKT TIAP 240

Qy    241  YSLRGRTHPTVAAPRTWAE LDDPALRQLSYDEV LTRIARDGDL LERLDADAPVADRLTRY 300
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Db    241  YSLRGRTHPTVAAPRTWAE LDDPALRQLSYDEV LTRIARDGDL LERLDADAPVADRLTRY 300

Qy    301  RMRDASKTPEPIPTAKPVTGDGNTFVIQEH HARRPHYDFRLECDGVLVSWAVPKNLP DN 360
      |||
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Qy    361  TSVNHLAINTEDHPLEYATFEGAIPSGEYGAGKV I I WDSGT YDTEKFHDDPHTGEVIVNL 420
      |||
Db    361  TSVNHLAINTEDHPLEYATFEGAIPSGEYGAGKV I I WDSGT YDTEKFHDDPHTGEVIVNL 420

Qy    421  HGRISGRYALIRTNGDRWLAHRLKNQKDQKVFEFDNLAPMLATHGT VAGLKASQWAFEG 480
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Qy    481  KWDGYRLLVEADHGAVRLRSRSGRDVTA EYPQLRALAEDLADHHVVLDGEAVVLDSSGVP 540
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Qy    541  SFSQMQRNGRDRTRVEFWAFD LLYLDGRALLGTRYQDRKKLETLANATSLTVP ELLPGDG 600
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Db 541 SFSQMQRGRDTRVEFWAFDLLYLDGRALLGTRYQDRRKLETLANATSLTVPELLPGDG 600  
 Qy 601 AQAFACSRKHGWEVIAKRRDSRYQPGRRCASWVKDKHWNTQEVVIGGWAGEGGRSSGV 660  
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 Db 661 GSLLMGIPGPGGLQFAGRVGTGLSERELANLKEMLAPLHTDESPFDVPLPARDAKGITYV 720  
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